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46

RAW SEQUENCE LISTING PATENT APPLICATION US/09/768,840

DATE: 03/15/2001 TIME: 22:39:47

INPUT SET: S36517.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

ENTERED SEQUENCE LISTING 1 2 General Information (1) 3 4 (i) APPLICANT: Hillman, Jennifer L. 5 Goli, Surya K. 6 7 (ii) TITLE OF THE INVENTION: NOVEL CALCIUM-BINDING 8 PROTEIN 9 10 (iii) NUMBER OF SEQUENCES: 4 11 12 (iv) CORRESPONDENCE ADDRESS: 13 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc. 14 (B) STREET: 3174 Porter Drive 15 (C) CITY: Palo Alto 16 (D) STATE: CA 17 (E) COUNTRY: USA 18 (F) ZIP: 94304 19 20 (v) COMPUTER READABLE FORM: 21 (A) MEDIUM TYPE: Diskette 22 (B) COMPUTER: IBM Compatible 23 (C) OPERATING SYSTEM: DOS 24 (D) SOFTWARE: FastSEQ for Windows Version 2.0 25 26 (vi) CURRENT APPLICATION DATA: 27 (A) APPLICATION NUMBER: 09/768,840 28 (B) FILING DATE: 29 (C) CLASSIFICATION: 30 31 (vii) PRIOR APPLICATION DATA: 32 (A) APPLICATION NUMBER: 09/206,499 33 34 (B) FILING DATE: 35 36 (viii) ATTORNEY/AGENT INFORMATION: 37 (A) NAME: Billings, Lucy J. 38 (B) REGISTRATION NUMBER: 36,749 39 (C) REFERENCE/DOCKET NUMBER: PF-0261 US 40 41 (ix) TELECOMMUNICATION INFORMATION: 42 (A) TELEPHONE: 415-855-0555 43 (B) TELEFAX: 415-845-4166 44 45

(2) INFORMATION FOR SEQ ID NO:1:

RAW SEQUENCE LISTING PATENT APPLICATION US/09/768,840

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INPUT SET: S36517.raw

```
47
            (i) SEQUENCE CHARACTERISTICS:
48
              (A) LENGTH: 328 amino acids
49
              (B) TYPE: amino acid
50
              (C) STRANDEDNESS: single
51
              (D) TOPOLOGY: linear
52
53
            (vii) IMMEDIATE SOURCE:
54
55
               (A) LIBRARY: CONUTUT01
               (B) CLONE: 2509570
57
58
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
59
      Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Leu Arg His
60
61
                      5
      Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly
62
63
                                      25
                  20
      Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala
64
65
                                  40
      His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val
66
67
                              55
      Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu
68
69
                          70
70
      Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp
71
      Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg
72
73
                                      105
      His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp
74
75
                                  120
                                                      125
      Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly
76
77
                              135
78
     His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr
79
                         150
                                              155
      Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp
80
81
                                         170
     Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu
82
83
                                     185
     His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr
84
85
                                  200
86
     Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu
87
                             215
     Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala
88
                                             235
89
                         230
     Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn
90
91
                     245 .
                                          250
     Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro
92
93
                 260
                                      265
     Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu
94
95
                                  280
     Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
96
97
                             295
     Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
98
99
                          310
                                              315
```

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Leu Thr Arg His His Asp Glu Leu
100
                       325
101
102
                (2) INFORMATION FOR SEQ ID NO:2:
103
104
             (i) SEQUENCE CHARACTERISTICS:
105
               (A) LENGTH: 1055 base pairs
106
               (B) TYPE: nucleic acid
107
               (C) STRANDEDNESS: single
108
               (D) TOPOLOGY: linear
109
110
             (vii) IMMEDIATE SOURCE:
111
                (A) LIBRARY: CONTUT01
112
                (B) CLONE: 2509570
113
114
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
115
116
       GGAGAGCGGA NGNANTGGNA TAACAGGGGA CCGATGATGT GGCGACCATC AGTTCTGCTG
                                                                               60
117
       CTTCTGTTGC TACTGAGGCA CGGGGCCCAG GGGAAGCCAT CCCCAGACGC AGGCCCTCAT
                                                                              120
118
      GGCCAGGGGA GGGTGCACCA GGCGGCCCCC CTGAGCGACG CTCCCCATGA TGACGCCCAC
                                                                              180
119
       GGGAACTTCC AGTACGACCA TGAGGCTTTC CTGGGACGGG AAGTGGCCAA GGAATTCGAC
                                                                              240
120
      CAACTCACCC CAGAGGAAAG CCAGGCCCGT CTGGGGCGGA TCGTGGACCG CATGGACCGC
                                                                              300
121
       GCGGGGGACG GCGACGCTG GGTGTCGCTG GCCGAGCTTC GCGCGTGGAT CGCGCACACG
                                                                              360
122
       CAGCAGCGGC ACATACGGGA CTCGGTGAGC GCGGCCTGGG ACACGTACGA CACGGACCGC
                                                                             . 420
123
       GACGGGCGTG TGGGTTGGGA GGAGCTGCGC AACGCCACCT ATGGCCACTA CGCGCCCGGT
                                                                              480
124
       GAAGAATTTC ATGACGTGGA GGATGCAGAG ACCTACAAAA AGATGCTGGC TCGGGACGAG
                                                                              540
125
       CGGCGTTTCC GGGTGGCCGA CCAGGATGGG GACTCGATGG CCACTCGAGA GGAGCTGACA
                                                                              600
126
       GCCTTCCTGC ACCCCGAGGA GTTCCCTCAC ATGCGGGACA TCGTGATTGC TGAAACCCTG
                                                                              660
127
       GAGGACCTGG ACAGAAACAA AGATGGCTAT GTCCAGGTGG AGGAGTACAT CGCGGATCTG
                                                                              720
128
       TACTCAGCCG AGCCTGGGGA GGAGGAGCCG GCGTGGGTGC AGACGGAGAG GCAGCAGTTC
                                                                              780
129
       CGGGACTTCC GGGATCTGAA CAAGGATGGG CACCTGGATG GGAGTGAGGT GGGCCACTGG
                                                                              840
130
       GTGCTGCCCC CTGCCCAGGA CCAGCCCCTG GTGGAAGCCA ACCACCTGCT GCACGAGAGC
                                                                              900
131
       GACACGGACA AGGATGGGCG GCTGAGCAAA GCGGAAATCC TGGGTAATTG GAACATGTTT
                                                                              960
132
       GTGGGCAGTC AGGCCACCAA CTATGGCGAG GACCTGACCC GGCACCACGA TGAGCTGTGA
                                                                             1020
133
                                                                             1055
       GCACCGCGCA CCTGCCACAG CCTCAGAGGC CCGCA
134
135
                (2) INFORMATION FOR SEQ ID NO:3:
136
137
             (i) SEQUENCE CHARACTERISTICS:
138
                (A) LENGTH: 331 amino acids
139
                (B) TYPE: amino acid
140
                (C) STRANDEDNESS: single
141
                (D) TOPOLOGY: linear
142
143
             (vii) IMMEDIATE SOURCE:
144
                 (A) LIBRARY: GenBank
145
                 (B) CLONE: 1262329
146
147
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
148
149
       Met Ala Arg Gly Gly Arg Gly Arg Leu Gly Leu Ala Leu Gly Leu
150
                                            10
                         5
151
       Leu Leu Ala Leu Val Leu Ala Pro Arg Val Leu Arg Ala Lys Pro Thr
```

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INPUT SET: S36517.raw

```
25
153
      Val Arg Lys Glu Arg Val Val Arg Pro Asp Ser Glu Leu Gly Glu Arg
154
                                  40
155
      Pro Pro Glu Asp Asn Gln Ser Phe Gln Tyr Asp His Glu Ala Phe Leu
156
157
      Gly Lys Glu Asp Ser Lys Thr Phe Asp Gln Leu Thr Pro Asp Glu Ser
158
                          70
                                              75
159
      Lys Glu Arg Leu Gly Lys Ile Val Asp Arg Ile Asp Asn Asp Gly Asp
160
                                           90
161
                      85
      Gly Phe Val Thr Thr Glu Glu Leu Lys Thr Trp Ile Lys Arg Val Gln
162
                                      105
163
                  100
      Lys Arg Tyr Ile Phe Asp Asn Val Ala Lys Val Trp Lys Asp Tyr Asp
164
                                 120
165
      Arg Asp Lys Asp Asp Lys Ile Ser Trp Glu Glu Tyr Lys Gln Ala Thr
166
                                                   140
                              135
167
      Tyr Gly Tyr Tyr Leu Gly Asn Pro Ala Glu Phe His Asp Ser Ser Asp
168
                                              155
                          150
169
      His His Thr Phe Lys Lys Met Leu Pro Arg Asp Glu Arg Arg Phe Lys
170
                                          170
                       165
171
      Ala Ala Asp Leu Asn Gly Asp Leu Thr Ala Thr Arg Glu Glu Phe Thr
172
       180
                                       185
173
      Ala Phe Leu His Pro Glu Glu Phe Glu His Met Lys Glu Ile Val Val
174
                                   200
              195
175
      Leu Glu Thr Leu Glu Asp Ile Asp Lys Asn Gly Asp Gly Phe Val Asp
176
                               215
177
      Gln Asp Glu Tyr Ile Ala Asp Met Phe Ser His Glu Glu Asn Gly Pro
178
                                               235
                           230
179
       Glu Pro Asp Trp Val Leu Ser Glu Arg Glu Gln Phe Asn Glu Phe Arg
180
                       245
                                           250
181
      Asp Leu Asn Lys Asp Gly Lys Leu Asp Lys Asp Glu Ile Arg His Trp
182
                                       265
183
      Ile Leu Pro Gln Asp Tyr Asp His Ala Gln Ala Glu Ala Arg His Leu
184
                                   280
185
              275
       Val Tyr Glu Ser Asp Lys Asn Lys Asp Glu Lys Leu Thr Lys Glu Glu
186
                               295
                                                   300
187
       Ile Leu Glu Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr
188
                                                                   320
                                               315
                           310
189
      Gly Glu Asp Leu Thr Lys Asn His Asp Glu Leu
190
                       325
191
192
                (2) INFORMATION FOR SEQ ID NO:4:
193
194
             (i) SEQUENCE CHARACTERISTICS:
195
               (A) LENGTH: 325 amino acids
               (B) TYPE: amino acid
197
               (C) STRANDEDNESS: single
198
               (D) TOPOLOGY: linear
199
200
             (vii) IMMEDIATE SOURCE:
201
                (A) LIBRARY: GenBank
202
                (B) CLONE: 220582
203
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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															_	
206 207	Met	Ala	Arq	Gly	Gly	Arg	Leu	Gly	Leu	Ala	Leu	Gly	Leu	Leu	Leu 15	Ala
208	1		_	_	5				_	10	1701	N rcr	Laze	Glu	Ara	Val
209	Leu	Val	Leu	Ala	Leu	Arg	Ala	Lys	Pro	Thr	Val	Arg	пуз	30	5	
210				20					25	3	Dro	Dro	Glu	Asp	Asn	Gln
211	Val	Arg	Pro	Asp	Ser	Glu	Leu	GIY	GIU	Arg	PIO	FIO	45			
212		_	35				-	40	Db	T 011	Clv	Tays	Glu	Asp	Ser	Lys
213	Ser	Phe	35 Gln	Tyr	Asp	His	Glu	Ala	Pne	ьeu	Gry	60	0			_
214		50				_	55	3	Clu	Cor	LVS	Glu	Arq	Leu	Gly	Lys
215	Thr	Phe	Asp	Gln	Leu	Ser	Pro	Asp	GIU	Ser	75		5		-	80
216	65		Asp			70		7.00	Glv	Δsn	Glv	Leu	Val	Thr	Thr	Glu
217	Ile	Val	Asp	Arg	Ile	Asp	ser	Asp	Gry	90	0-1				95	
218			Lys	_	85	-1 -	Tare	λνα	Va 1	Gln	Lvs	Arg	Tyr	Ile	Tyr	Asp
219	Glu	Leu	Lys	Leu	Trp	116	гур	Arg	105	U		_		110		
220		_		100	7701	ш×п	Lvc	Δsp	Tvr	Asp	Arg	Asp	Lys	Asp	Glu	Lys
221	Asn	Val	Ala	гЛа	Val	пр	пур	120	-1-	-	_		125			_
222			115	a1.,	Clu	ጥነ/ነገ	Lvs	Gln	Ala	Thr	Tyr	Gly	Tyr	Tyr	Leu	Gly
223	Ile	ser	Trp	GIU	GIU	- y -	135					140				
224		130	717	Glu	Phe	His	Asp	Ser	Ser	Asp) His	His	Thr	Phe	Lys	Lys 160
225	Asn	Pro	Ala	GIU	FIIC	150					155				_	160
226	145	T 0.1	Bro	λνα	Δςη	Glu	Arq	Arg	Phe	Lys	: Ala	Ser	Asp) Leu	Asp	Gly
227	Met	. ьес	PIO	Arg	165	-		_		170)		_		175	
228	7 0 0	T.01	Thr	Δla	Thr	Arq	Glu	Glu	Phe	Thi	: Ala	Phe	Leu	1 H15	PIC	Glu
229	ASL) LIEU		180)				185	5			1	190) . (1)	, Aen
230	Gla	. Phe	Glu	His	Met	Lys	Glu	ı Ile	val	. Va.	l Lev	GIU	LUI	- пес	I GI	a Asp
231 232	GIU		195	5		_		200) _			•	205) , Път	- T]4	ala
232	Tle	Ast	LVS	Asr	ı Gly	Asp	Gly	/ Phe	val	L As	o G11	ASI) GT	и туг		e Ala
234		210	· 1				215	5		_	- 01.	220) - 701	ח ידיי	o Va	l Leu
235	Ast	Me	t Phe	e Sei	: His	: Gli	ı Ası) Ası	ı GI	y Pro	23!	- 1 PIC	נפא כ	P 1-1		Leu 240
236	225	5				230)	_	1	- 7.00	∠3: ~ 7.01	ס ה ד.בו	1 ASI	n Lv:	s As	o Gly
237	Sei	r Gl	u Arg	g Glu	ı Glı	ı Phe	e Ası	n Ası	o Pne	25	g Abj	ישם ק	4 110.		25	p Gly 5
238					245	5		3	114	25 77	n Tl	e Tier	ı Pr	o Gl	n As	p Tyr
239	Ly	s Le	u Asj	o Liya	s Ası	o GT	1 110	e Ar	26	5 11	P			27	0	
240				26	0	~3		~ 7\ *	20 11 ~	o T.e	u Va	l Tv	r Gl	u Se	r As	p Lys
241	As	p Hi	s Ala	a Gl	n Ala	a GI	u AI	a Ary	0 111	5 110	<u>.</u>	1	28	5		
242			27	5			. mh		o e G1	11 Gl	u Il	e Le	u As	p As	n Tr	p Asn
243	As	n Ly	s As	b GT	u Me	с те	u 111 29	2 - 11	5 01			30	0			
244		29	0		0.	~ ~1	22 21	э a Th	r As	n Tv	r Gl	y Gl	u As	p Le	u Th	r Lys 320
245			e Va	I GI	у ѕе	r Gi 31	יי יי עד			1	31	5				320
246	30			aı	T.O		•									
247	As	n Hi	s As	b ет	и ве 32	և 5			•							
248					34	_										
249																

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SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/09/768,840

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